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(1) GENERAL INFORMATION:

    (i) APPLICANT:
        SOUPPE, Jerome
        BEUDEKER, Robert Franciscus

    (ii) TITLE OF INVENTION:
        PROCESS FOR THE PRODUCTION OF ALCOHOLIC BEVERAGES USING MALTSEED

    (iii) NUMBER OF SEQUENCES: 8

    (iv) CORRESPONDENCE ADDRESS:
        (A)   ADDRESSEE: LADAS & PARRY
        (B)   STREET: 26 WEST 61 STREET
        (C)   CITY   NEW YORK
        (D)   STATE   NY
        (E)   ZIP CODE: 10023
        (F)   COUNTRY: USA

    (iv) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM   PC compatible
        (C) OPERATING SYSTEM: Microsoft Windows for Workgroups
        (D) SOFTWARE: WordPerect 8

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: 09/970,616
        (B) FILING DATE: 04-OCT-2001
        (C) CLASSIFICATION: 435

    (vi) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: 09/230,590
        (B) FILING DATE: 28-APR-1999

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: PCT/EP97/04016
        (B) FILING DATE: 23-JUL-1997

    (vi) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: EP 96202195.2
        (B) FILING DATE: 05-AUG-1996

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: MASS, CLIFFORD J.
        (B) REGISTRATION NO. 30,086
        (C) REF./DOCKET NO.: U-012094-9

    (ix) TELECOMMUNICATION INFORMATION:
        (A)   TELEPHONE NUMBER: (212) 708-1890
        (B)   TELEFAX NUMBER: (212) 246-8959
        (C)   TELEX NUMBER: 233288

(2) INFORMATION FOR SEQ ID NO: 1:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 557 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: cDNA

      (iii) HYPOTHETICAL: NO

      (iii) ANTI-SENSE: NO

      (ix) FEATURE:
          (A) NAME/KEY: CDS
          (B) LOCATION: 1..555
          (D) OTHER INFORMATION: /product= "mature protein"

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
ATG AGC GCG GGA ATC AAC TAC GTC CAG AAC TAC AAT GGC AAC CTC GGC        48
Met Ser Ala Gly Ile Asn Tyr Val Gln Asn Tyr Asn Gly Asn Leu Gly
 1               5                  10                  15

GAC TTT ACT TAC GAC GAG TCA GCG GGA ACT TTC AGC ATG TAT TGG GAG        96
Asp Phe Thr Tyr Asp Glu Ser Ala Gly Thr Phe Ser Met Tyr Trp Glu
                20                  25                  30

GAT GGC GTG TCC TCA GAC TTC GTC GTG GGA CTG GGC TGG ACC ACT GGA       144
Asp Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Trp Thr Thr Gly
                35                  40                  45

TCA TCC AAT GCG ATC ACC TAC AGC GCC GAG TAC TCC GCG TCA GGA TCA       192
Ser Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser
        50                  55                  60

GCC TCC TAT CTG GCC GTG TAC GGA TGG GTG AAC TAC CCG CAG GCC GAG       240
Ala Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gln Ala Glu
 65                  70                  75                  80

TAC TAC ATC GTG GAG GAT TAC GGA GAT TAC AAC CCA TGC AGC TCA GCG       288
Tyr Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala
                    85                  90                  95

ACC TCC CTC GGA ACT GTG TAC AGC GAC GGC TCC ACC TAC CAG GTC TGC       336
Thr Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys
                100                 105                 110

ACC GAC ACC CGC ACT AAC GAG CCG TCA ATC ACC GGC ACT TCC ACC TTC       384
Thr Asp Thr Arg Thr Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe
                115                 120                 125
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ACC CAG TAC TTC AGC GTG CGC GAG TCC ACT CGC ACC TCA GGA ACC GTG          432
Thr Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val
    130             135             140

ACC GTC GCG AAC CAC TTC AAC TTC TGG GCG CAG CAC GGA TTC GGC AAC          480
Thr Val Ala Asn His Phe Asn Phe Trp Ala Gln His Gly Phe Gly Asn
145             150             155             160

AGC GAC TTT AAC TAC CAG GTG GTC GCA GTG GAG GCA TGG TCA GGA GCG          528
Ser Asp Phe Asn Tyr Gln Val Val Ala Val Glu Ala Trp Ser Gly Ala
            165             170             175

GGC TCA GCG TCC GTC ACT ATC AGC TCC TG                                   557
Gly Ser Ala Ser Val Thr Ile Ser Ser
        180             185
```

(2) INFORMATION FOR SEQ ID NO: 2:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 185 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ser Ala Gly Ile Asn Tyr Val Gln Asn Tyr Asn Gly Asn Leu Gly
1               5               10              15

Asp Phe Thr Tyr Asp Glu Ser Ala Gly Thr Phe Ser Met Tyr Trp Glu
            20              25              30

Asp Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Trp Thr Thr Gly
            35              40              45

Ser Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser
    50              55              60

Ala Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gln Ala Glu
65              70              75              80

Tyr Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala
            85              90              95

Thr Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys
            100             105             110

Thr Asp Thr Arg Thr Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe
        115             120             125

Thr Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val
    130             135             140
```

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Thr Val Ala Asn His Phe Asn Phe Trp Ala Gln His Gly Phe Gly Asn
145   150   155   160

Ser Asp Phe Asn Tyr Gln Val Val Ala Val Glu Ala Trp Ser Gly Ala
                165   170   175

Gly Ser Ala Ser Val Thr Ile Ser Ser
            180   185

(2) INFORMATION FOR SEQ ID NO: 3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 71 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA

        (iii) HYPOTHETICAL: NO

        (iii) ANTI-SENSE: NO

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Nicotiana tabacum

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AACTTCCTCA AGAGCTTCCC CTTTTATGCC TTCCTTTGTT TTGGCCAATA CTTTGTAGCT   60

GTTACGCATG C   71

(2) INFORMATION FOR SEQ ID NO: 4:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 80 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA

        (iii) HYPOTHETICAL: NO

        (iii) ANTI-SENSE: YES

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CCATGGCATG CGTAACAGCT ACAAAGTATT GGCCAAAACA AAGGAAGGCA TAAAAGGGGA   60

AGCTCTTGAG GAAGTTCATG   80

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (iii) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGGATGGCA TGCTGTTGTA G   21

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (iii) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCACAATTCT CGAGGAGACC G   21

(2) INFORMATION FOR SEQ ID NO: 7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (iii) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCTCTTAAGG ATCCAATGCG G   21

(2) INFORMATION FOR SEQ ID NO: 8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (iii) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CTTATCTGAA TTCGGAAGCT C   21